

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/756,213A
Source: 1FW/6
Date Processed by STIC: 3/2/07

ENTERED



IFW16

RAW SEQUENCE LISTING

DATE: 03/02/2007

PATENT APPLICATION: US/10/756,213A

TIME: 10:59:41

Input Set : A:\SEQLIST.TXT

Output Set: N:\CRF4\03022007\J756213A.raw

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4 <110> APPLICANT: GOOD, Allen G.
5   STROEHER, Virginia L.
6   MUENCH, Douglas G.
8 <120> TITLE OF INVENTION: PLANTS WITH ENHANCED LEVELS OF NITROGEN
9   UTILIZATION PROTEINS IN THEIR ROOT EPIDERMIS AND USES
10  THEREOF
12 <130> FILE REFERENCE: 595792000420
14 <140> CURRENT APPLICATION NUMBER: 10/756,213A
15 <141> CURRENT FILING DATE: 2004-01-12
17 <150> PRIOR APPLICATION NUMBER: 10/321,718
18 <151> PRIOR FILING DATE: 2002-12-17
20 <150> PRIOR APPLICATION NUMBER: 09/493,803
21 <151> PRIOR FILING DATE: 2000-01-28
23 <160> NUMBER OF SEQ ID NOS: 3
25 <170> SOFTWARE: FastSEQ for Windows Version 4.0
27 <210> SEQ ID NO: 1
28 <211> LENGTH: 365
29 <212> TYPE: DNA
30 <213> ORGANISM: Brassica napus
32 <400> SEQUENCE: 1
33 gtcgacctgc aggtcaacgg atcctaatacg gggatatatcc cgaccocggaa aaagaaacgt 60
34 aggacacgtg acaaaaacttc atatgatccg agtgaatcaa gccaaaaggg ggattgacac 120
35 aacagctcag ctttcgtttt cgggtccaatc gctgttccaa ctttacttac aagtcgtaca 180
36 cgtctctctc tctctctctc tctctcactc acttctcttt ataaagactc tctgatcaaa 240
37 cgtataatcg gaaaactcca ttctttgata ccacgataa tactaagaga ggtgattgat 300
38 tctttaatca ctgtttgata tctttaactt tgatccattt actctgttca atcatttttg 360
39 tagag 365
41 <210> SEQ ID NO: 2
42 <211> LENGTH: 1701
43 <212> TYPE: DNA
44 <213> ORGANISM: Barley
46 <220> FEATURE:
47 <221> NAME/KEY: CDS
48 <222> LOCATION: (95)...(1540)
50 <400> SEQUENCE: 2
51 ggccacaaaa ccgcggaaag agatagacgg acagctagag gcgtcggaag atactcgctg 60
52 ctctgcgcgc ccttcgtct tagttgatct cgcc atg gct gcc acc gtc gcc gtg 115
53 Met Ala Ala Thr Val Ala Val
54 1 5
56 gac aac ctg aac ccc aag gtt tta aaa tgt gag tat gct gtg cgt gga 163
57 Asp Asn Leu Asn Pro Lys Val Leu Lys Cys Glu Tyr Ala Val Arg Gly
58 10 20
60 gag att gtc atc cat gct cag cgc ttg cag gaa cag cta aag act caa 211

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61 Glu Ile Val Ile His Ala Gln Arg Leu Gln Glu Gln Leu Lys Thr Gln
62      25              30              35
64 cca ggg tct cta cct ttt gat gag atc ctc tat tgt aac att ggg aac 259
65 Pro Gly Ser Leu Pro Phe Asp Glu Ile Leu Tyr Cys Asn Ile Gly Asn
66 40      45              50              55
68 cca caa tct ctt ggt cag caa cca gtt aca ttc ttc agg gag gtt ctt 307
69 Pro Gln Ser Leu Gly Gln Gln Pro Val Thr Phe Phe Arg Glu Val Leu
70      60              65              70
72 gcc ctt tgt gat cat cca gac ctg ttg caa aga gag gaa atc aaa aca 355
73 Ala Leu Cys Asp His Pro Asp Leu Leu Gln Arg Glu Glu Ile Lys Thr
74      75              80              85
76 ttg ttc agt gct gat tct att tct cga gca aag cag att ctt gcc atg 403
77 Leu Phe Ser Ala Asp Ser Ile Ser Arg Ala Lys Gln Ile Leu Ala Met
78      90              95              100
80 ata cct gga aga gca aca gga gca tac agc cat agc cag ggt att aaa 451
81 Ile Pro Gly Arg Ala Thr Gly Ala Tyr Ser His Ser Gln Gly Ile Lys
82 105      110              115
84 gga ctt cgt gat gca att gct tct ggg atc gct tca cga gat gga ttc 499
85 Gly Leu Arg Asp Ala Ile Ala Ser Gly Ile Ala Ser Arg Asp Gly Phe
86 120      125              130              135
88 cct gct aat gct gat gac att ttt ctc aca gat gga gca agt cct ggg 547
89 Pro Ala Asn Ala Asp Asp Ile Phe Leu Thr Asp Gly Ala Ser Pro Gly
90      140              145              150
92 gtg cac ctg atg atg caa tta ctg ata agg aat gag aaa gat ggc att 595
93 Val His Leu Met Met Gln Leu Leu Ile Arg Asn Glu Lys Asp Gly Ile
94      155              160              165
96 ctt gtc ccg att cct cag tac ccc ttg tac tcg gct tcc ata gct ctt 643
97 Leu Val Pro Ile Pro Gln Tyr Pro Leu Tyr Ser Ala Ser Ile Ala Leu
98      170              175              180
100 cat ggc gga gct ctt gtc cca tac tat ctc aat gaa tcg acg ggc tgg 691
101 His Gly Gly Ala Leu Val Pro Tyr Tyr Leu Asn Glu Ser Thr Gly Trp
102 185      190              195
104 ggt ttg gaa acc tct gat gtt aag aag caa ctt gaa gat gct cgg tca 739
105 Gly Leu Glu Thr Ser Asp Val Lys Lys Gln Leu Glu Asp Ala Arg Ser
106 200      205              210              215
108 aga ggc atc aac gtt agg gct ttg gtg gtt atc aat cca gga aat cca 787
109 Arg Gly Ile Asn Val Arg Ala Leu Val Val Ile Asn Pro Gly Asn Pro
110      220              225              230
112 act gga cag gta ctt gct gaa gaa aac caa tat gac ata gtg aag ttc 835
113 Thr Gly Gln Val Leu Ala Glu Glu Asn Gln Tyr Asp Ile Val Lys Phe
114      235              240              245
116 tgc aaa aat gag ggt ctt gtt ctt cta gct gat gag gta tac caa gag 883
117 Cys Lys Asn Glu Gly Leu Val Leu Leu Ala Asp Glu Val Tyr Gln Glu
118      250              255              260
120 aac atc tat gtt gac aac aag aaa ttc cac tct ttc aag aag ata gtg 931
121 Asn Ile Tyr Val Asp Asn Lys Lys Phe His Ser Phe Lys Lys Ile Val
122      265              270              275
124 aga tcc ttg gga tac ggc gag gag gat ctc cct cta gta tca tat caa 979
125 Arg Ser Leu Gly Tyr Gly Glu Glu Asp Leu Pro Leu Val Ser Tyr Gln

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126 280          285          290          295
128 tct gtt tct aag gga tat tat ggt gag tgt ggt aaa aga ggt ggt tac 1027
129 Ser Val Ser Lys Gly Tyr Tyr Gly Glu Cys Gly Lys Arg Gly Gly Tyr
130          300          305          310
132 ttt gag att act ggc ttc agt gct cca gta aga gag cag atc tac aaa 1075
133 Phe Glu Ile Thr Gly Phe Ser Ala Pro Val Arg Glu Gln Ile Tyr Lys
134          315          320          325
136 ata gca tca gtg aac cta tgc tcc aat atc act ggc cag atc ctt gct 1123
137 Ile Ala Ser Val Asn Leu Cys Ser Asn Ile Thr Gly Gln Ile Leu Ala
138          330          335          340
140 agt ctt gtc atg aac cca cca aag gct agt gat gaa tca tac gct tca 1171
141 Ser Leu Val Met Asn Pro Pro Lys Ala Ser Asp Glu Ser Tyr Ala Ser
142          345          350          355
144 tac aag gca gaa aaa gat gga atc ctc gca tct tta gct cgt cgt gcg 1219
145 Tyr Lys Ala Glu Lys Asp Gly Ile Leu Ala Ser Leu Ala Arg Arg Ala
146 360          365          370          375
148 aag gca ttg gag cat gca ttc aat aaa ctt gag gga att act tgc aac 1267
149 Lys Ala Leu Glu His Ala Phe Asn Lys Leu Glu Gly Ile Thr Cys Asn
150          380          385          390
152 gag gct gaa gga gca atg tac gtg ttc cct caa atc tgt ctg cca cag 1315
153 Glu Ala Glu Gly Ala Met Tyr Val Phe Pro Gln Ile Cys Leu Pro Gln
154          395          400          405
156 aag gca att gag gct gct aaa gct gct aac aaa gca cct gat gca ttc 1363
157 Lys Ala Ile Glu Ala Ala Lys Ala Ala Asn Lys Ala Pro Asp Ala Phe
158          410          415          420
160 tat gct ctt cgt ctc ctc gag tcg act gga atc gtc gtt gtc cct gga 1411
161 Tyr Ala Leu Arg Leu Leu Glu Ser Thr Gly Ile Val Val Val Pro Gly
162          425          430          435
164 tca gga ttt ggc cag gtt cct ggc aca tgg cac ttc agg tgc acg atc 1459
165 Ser Gly Phe Gly Gln Val Pro Gly Thr Trp His Phe Arg Cys Thr Ile
166 440          445          450          455
168 ctt ccg cag gag gat aag atc ccg gca gtc atc tcc cgc ttc acg gtg 1507
169 Leu Pro Gln Glu Asp Lys Ile Pro Ala Val Ile Ser Arg Phe Thr Val
170          460          465          470
172 ttc cat gag gcg ttc atg tca gag tat cgt gac taaactggtg caacatgtgg 1560
173 Phe His Glu Ala Phe Met Ser Glu Tyr Arg Asp
174          475          480
176 gattacatac aaccctcatg gggttttcgt aggcgttctt gggttttgcct cccccccct 1620
177 tctctctctc tctctctctg acagcatcct cctctagatg agacaaaata aagcaaagcc 1680
178 atgtcatcct taaaaaaaaa a 1701
180 <210> SEQ ID NO: 3
181 <211> LENGTH: 482
182 <212> TYPE: PRT
183 <213> ORGANISM: Barley
185 <400> SEQUENCE: 3
186 Met Ala Ala Thr Val Ala Val Asp Asn Leu Asn Pro Lys Val Leu Lys
187 1          5          10          15
188 Cys Glu Tyr Ala Val Arg Gly Glu Ile Val Ile His Ala Gln Arg Leu
189          20          25          30

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190 Gln Glu Gln Leu Lys Thr Gln Pro Gly Ser Leu Pro Phe Asp Glu Ile
191      35      40      45
192 Leu Tyr Cys Asn Ile Gly Asn Pro Gln Ser Leu Gly Gln Gln Pro Val
193      50      55      60
194 Thr Phe Phe Arg Glu Val Leu Ala Leu Cys Asp His Pro Asp Leu Leu
195 65      70      75      80
196 Gln Arg Glu Glu Ile Lys Thr Leu Phe Ser Ala Asp Ser Ile Ser Arg
197      85      90      95
198 Ala Lys Gln Ile Leu Ala Met Ile Pro Gly Arg Ala Thr Gly Ala Tyr
199      100     105     110
200 Ser His Ser Gln Gly Ile Lys Gly Leu Arg Asp Ala Ile Ala Ser Gly
201      115     120     125
202 Ile Ala Ser Arg Asp Gly Phe Pro Ala Asn Ala Asp Asp Ile Phe Leu
203      130     135     140
204 Thr Asp Gly Ala Ser Pro Gly Val His Leu Met Met Gln Leu Leu Ile
205 145     150     155     160
206 Arg Asn Glu Lys Asp Gly Ile Leu Val Pro Ile Pro Gln Tyr Pro Leu
207      165     170     175
208 Tyr Ser Ala Ser Ile Ala Leu His Gly Gly Ala Leu Val Pro Tyr Tyr
209      180     185     190
210 Leu Asn Glu Ser Thr Gly Trp Gly Leu Glu Thr Ser Asp Val Lys Lys
211      195     200     205
212 Gln Leu Glu Asp Ala Arg Ser Arg Gly Ile Asn Val Arg Ala Leu Val
213      210     215     220
214 Val Ile Asn Pro Gly Asn Pro Thr Gly Gln Val Leu Ala Glu Glu Asn
215 225     230     235     240
216 Gln Tyr Asp Ile Val Lys Phe Cys Lys Asn Glu Gly Leu Val Leu Leu
217      245     250     255
218 Ala Asp Glu Val Tyr Gln Glu Asn Ile Tyr Val Asp Asn Lys Lys Phe
219      260     265     270
220 His Ser Phe Lys Lys Ile Val Arg Ser Leu Gly Tyr Gly Glu Glu Asp
221      275     280     285
222 Leu Pro Leu Val Ser Tyr Gln Ser Val Ser Lys Gly Tyr Tyr Gly Glu
223      290     295     300
224 Cys Gly Lys Arg Gly Gly Tyr Phe Glu Ile Thr Gly Phe Ser Ala Pro
225 305     310     315     320
226 Val Arg Glu Gln Ile Tyr Lys Ile Ala Ser Val Asn Leu Cys Ser Asn
227      325     330     335
228 Ile Thr Gly Gln Ile Leu Ala Ser Leu Val Met Asn Pro Pro Lys Ala
229      340     345     350
230 Ser Asp Glu Ser Tyr Ala Ser Tyr Lys Ala Glu Lys Asp Gly Ile Leu
231      355     360     365
232 Ala Ser Leu Ala Arg Arg Ala Lys Ala Leu Glu His Ala Phe Asn Lys
233      370     375     380
234 Leu Glu Gly Ile Thr Cys Asn Glu Ala Glu Gly Ala Met Tyr Val Phe
235 385     390     395     400
236 Pro Gln Ile Cys Leu Pro Gln Lys Ala Ile Glu Ala Ala Lys Ala Ala
237      405     410     415
238 Asn Lys Ala Pro Asp Ala Phe Tyr Ala Leu Arg Leu Leu Glu Ser Thr

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[illegible]

VERIFICATION SUMMARY

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Input Set : A:\SEQLIST.TXT

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